*Fig. 1*

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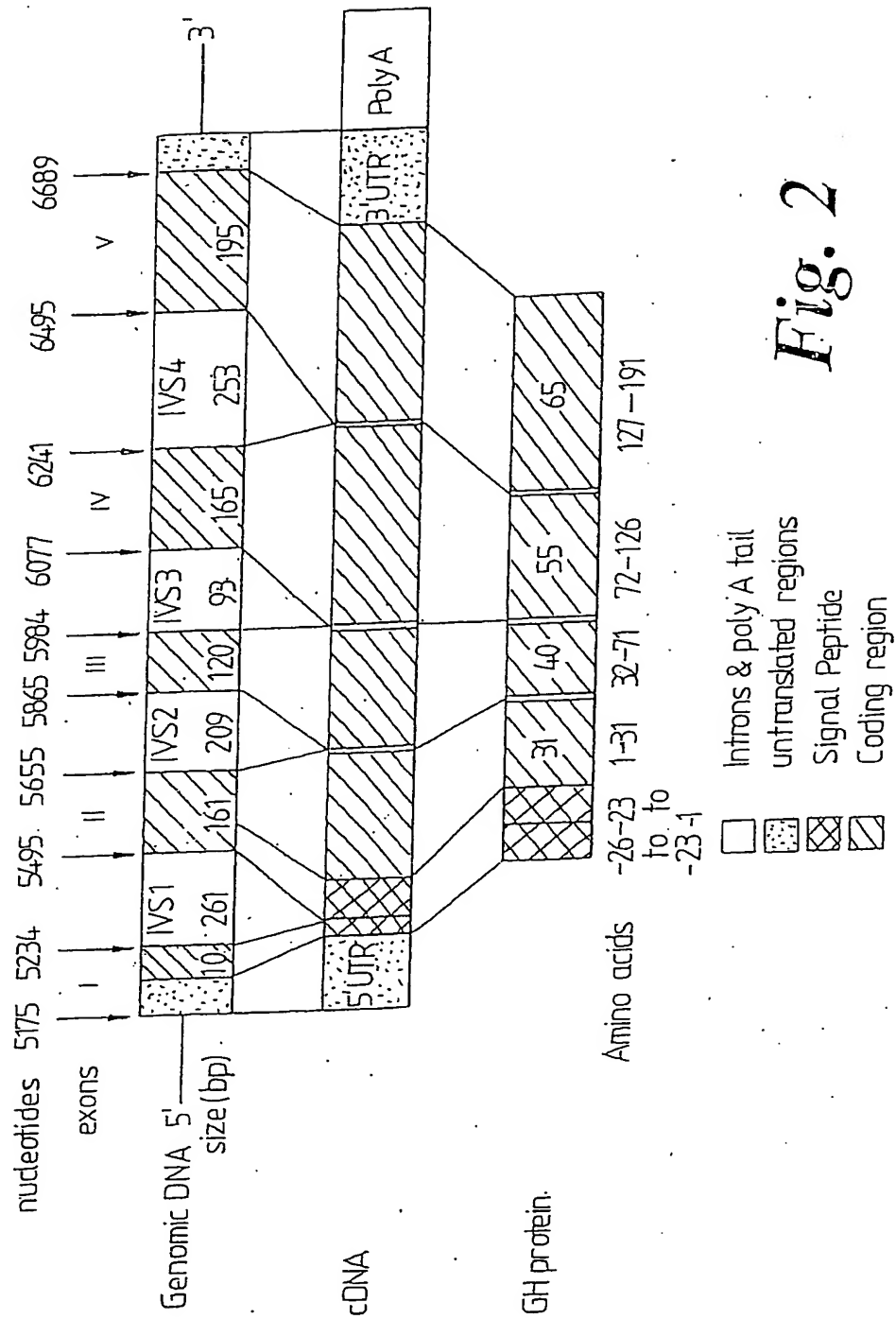


Fig. 2

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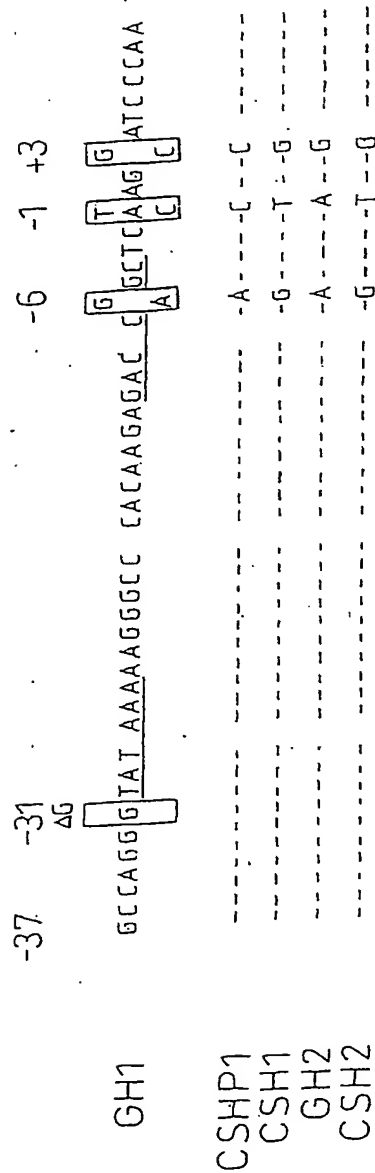
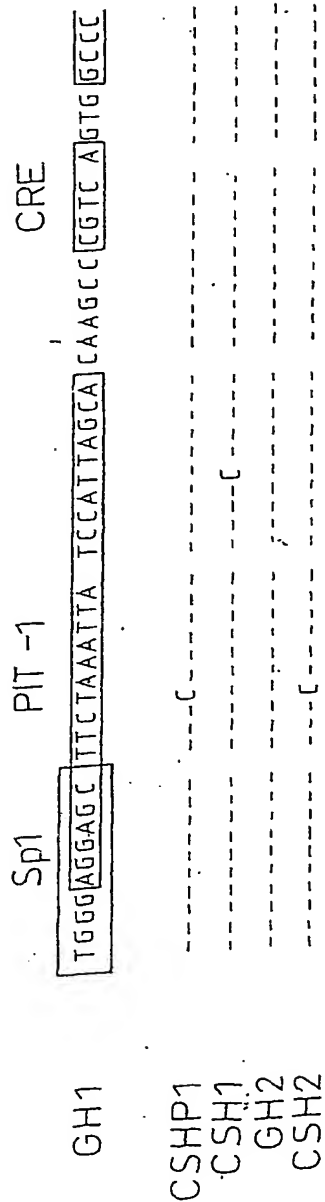


Fig. 3

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FIGURE 4

-700 ctgtttcttg gtttggtct ctgctgcaag tccaaggagc tggggcaata -651
-650 ccttgagct ggggtctctg tcccaggga cctgggggag cccagcaat -601
-600 gctcaggga agggagagc aaagtgtgg gttggtctc tctagtgtc -551
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-200 tcacaact ggtgacgtg ggaaggga gatacaga cagggggcat -151
-150 gatccagca tgtgtggag gagctctaa attatcatt agcacaagc -101
-100 cgtcagttgc ccatgcata aatgtacaca gaaacaggtg ggggcaacag -51
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+2951 gttactaac ccgagctacg ctgggtgctt ctttctacc acfttctta +3000

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FIGURE 5

Growth hormone 1

Gene symbol : GH1

Location : 17q

	1	2	
-26	ATG GCT ACA G↓GC TCC CGG ACG TCC CTG CTC CTG GCT TTT GGC CTG	-12	
	Met Ala Thr G ly Ser Arg Thr Ser Leu Leu Ala Phe Gly Leu		
-11	CTC TGC CTG CCC TGG CTT CAA GAG GGC AGT GCC TTC CCA ACC ATT	4	
	Leu Cys Leu Pro Trp Leu Gln Glu Gly Ser Ala Phe Pro Thr Ile		
5	CCC TTA TCC AGG CTT TTT GAC AAC GCT ATG CTC CGC GCC CAT CGT	19	
	Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu Arg Ala His Arg		
		2 3	
20	CTG CAC CAG CTG GCC TTT GAC ACC TAC CAG GAG TTT ↓ GAA GAA GCC	34	
	Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe Glu Ala		
35	TAT ATC CCA AAG GAA CAG AAG TAT TCA TTC CTG CAG AAC CCC CAG	49	
	Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro Gln		
50	ACC TCC CTC TGT TTC TCA GAG TCT ATT CCG ACA CCC TCC AAC AGG	64	

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Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg

3 4

65 GAG GAA ACA CAA CAG AAA TCC ↓ AAC CTA GAG CTG CTC CGC ATC TCC 79

Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser

80 CTG CTG CTC ATC CAG TCG TGG CTG GAG CCC GTG CAG TTC CTC AGG 94

Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg

95 AGT GTC TTC GCC AAC AGC CTG GTG TAC GGC GCC TCT GAC AGC AAC 109

Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn

110 GTC TAT GAC CTC CTA AAG GAC CTA GAG GAA GGC ATC CAA ACG CTG 124

Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu

4 5

125 ATG GGG ↓ AGG CTG GAA GAT GGC AGC CCC CGG ACT GGG CAG ATC TTC 139

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140 AAG CAG ACC TAC AGC AAG TTC GAC ACA AAC TCA CAC AAC GAT GAC 154

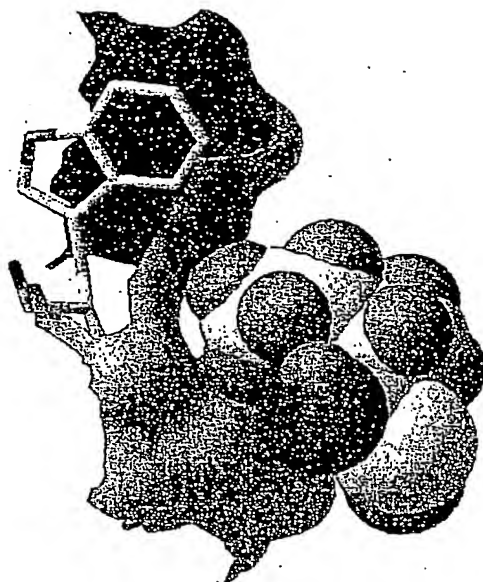
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155 GCA CTA CTC AAG AAC TAC GGG CTG CTC TAC TGC TTC AGG AAG GAC 169
Ala Leu Leu Lys Lys Asn Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp

170 ATG GAC AAG GTC GAG ACA TTC CTG CGC ATC GTG CAG TGC CGC TCT 184
Met Asp Lys Val Glu Thr Phe Leu Arg Ile Val Gln Cys Arg Ser

185 GTG GAG GGC AGC TGT GGC TTC TAG
Val Glu Gly Ser Cys Gly Phe *

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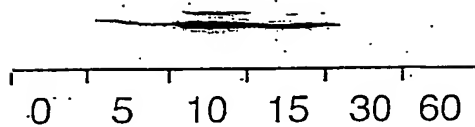
The tight interaction between the side chain of GH residue Ile179 and GHR residue Trp169.

The Ile179 residue is depicted by a space filling model. Trp169 is represented as a stick model, whilst the molecular surface of GHR residues 167-169 is shown in green

FIGURE 6

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A ERK



B STAT5

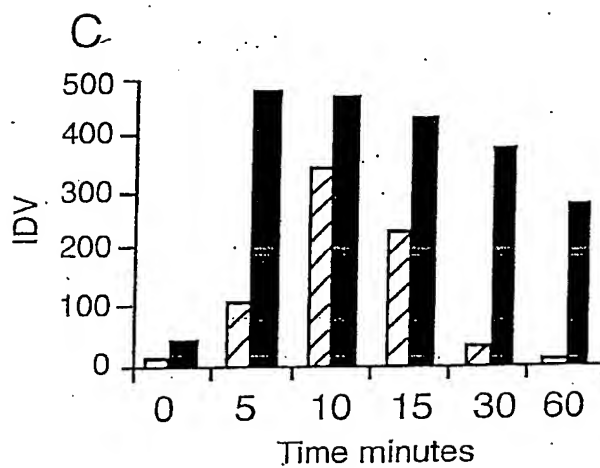
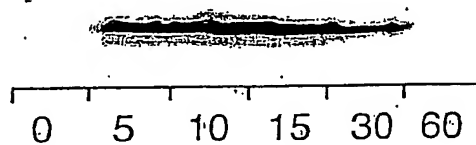


FIGURE 7

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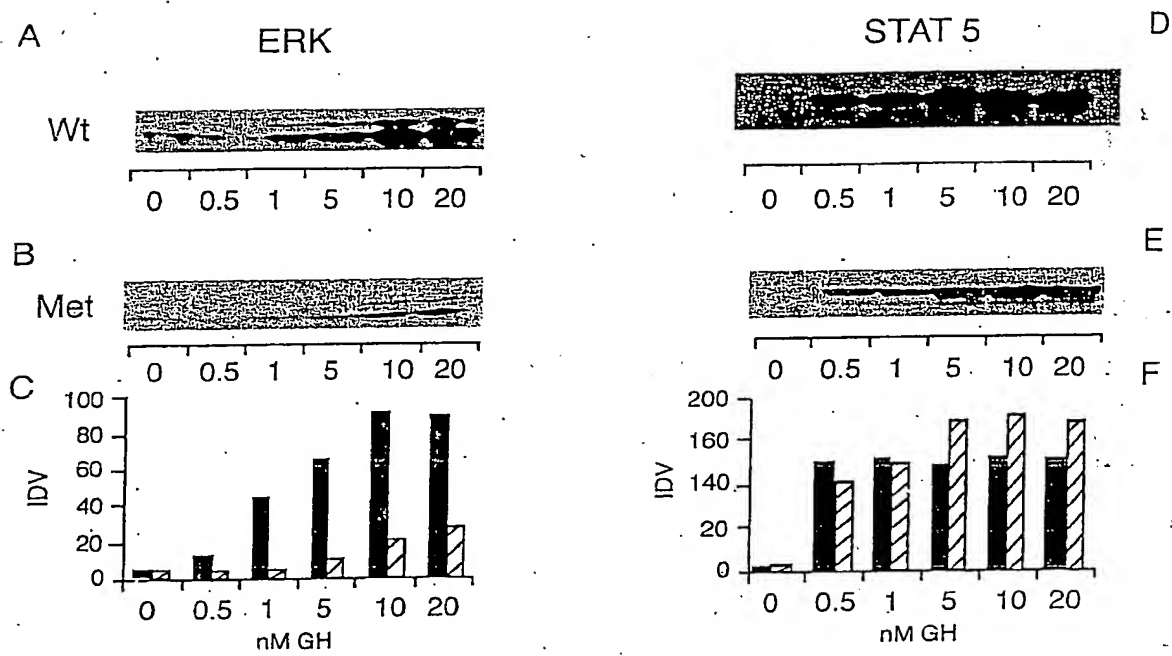


FIGURE 8

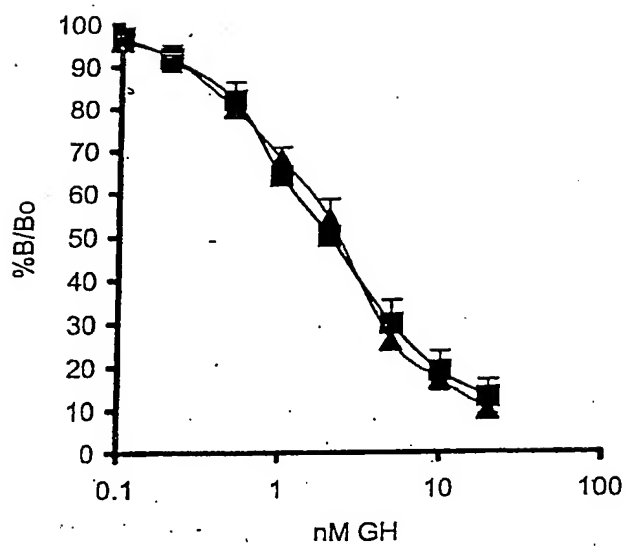


FIGURE 9

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